

FIGURE 1

TABLE 1

Exon-Intron Boundary Sequences of the Human alpha-7 nAChR Subunit Gene

Exon Number	Exon length (bp)	cDNA position	splice acceptor	flanking exon sequence	splice donor	Intron number	Intron Size approximate (Kb)
1	55	1-55		...CTG CAC G	GTAAAGCCAC	1	0.3
2	140	56-195	TCTCCTTAAG	TG TCC.....GAC GTG L H V S D V	GTGAGTCCCG	2	Unknown
3	45	196-240	TTTTTTGAAG	GAT GAG.....CAA ATG D E Q M	GTAAGTTAAG	3	9.0
4	110	241-350	TGTGTGTCAG	TCT TGG.....AAC AG S W N S	GTAAGCATAT	4	Unknown
5	80	351-430	CTGTTTCTAG	T GCT GAT.....CCT CCA G A D P P	GTAAGCTGCA	5	4.0
6	168	431-598	ACCCACACAG	GC ATA.....CTA GTG G G I L V	GTAAGCCATG	6	1.0
7	195	599-793	CCCTATGGAG	GA ATC.....TCC CTG G G I S L	GTAAGCGCCC	7	1.0
8	87	794-880	TATGTTTTAG	GG ATA.....TTG ATA G G I L I	GTAAGGCAAG	8	3.5
9	110	881-990	CTCTCCACAG	CC CAG.....AAG TGG A Q K W	GTACGTTCTT	9	5.0
10	519	991-1509	GTCTCCCCAG	ACC AGA... T R			

FIGURE 2

TABLE 2
Sequence Variants Identified in Full-Length and Duplicated Genomic Clones

DNA	EXONS CONT.	EXON 6 +/- 497-498	EXON 7 654	EXON 7 690	EXON 10 1269	EXON 10 1335	L76630
CHR15 HYBRID	5-10 1-10	+TG -TG			C/C		6GT 8GT
YAC							
D-948a10	5-10	-TG	T				6GT
D-853b12	6-10	-TG	T	A	C		6GT
D/F	5-10						
969b11	1-10	+TG -TG	C/T	G/A	C/T	C/C	6GT 8GT
F-134h10	1-10	+TG	C				8GT
F-776a12	1-10	+TG	C				8GT
F-791e6	1-10	+TG	C				8GT
F-811b6	1-10	+TG	C				8GT
F-953g6	1-10	+TG	C				8GT
F-859c11	1-10	+TG	C				8GT
F-810f11	1-10	+TG	C				8GT
F-801e1	1-10	+TG	C				8GT
BAC							
F-467o18	1-10	+TG	C				8GT

DNA	Control #	EXON 6 +/- 497-498	EXON 7 654	EXON 7 690	EXON 10 1269	EXON 10 1335
Control Genomic DNA	43	+/+ 10 +/- 33 -/- 0	C/C 5 C/T 38 T/T 0	G/G 0 G/A 43 A/A 0	C/C 6 C/T 36 T/T 1	C/C 24 C/T 19 T/T 0

FIGURE 3

TABLE 3
Expression Analysis of Sequence Variants

Subj	Bases 497-498			Base 654			Base 690			Base 933			Base 1296			Base 1335		
	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA
SL061	+/-	+	+/-	CT	C	CT	GA	G	GA	G	G	G	CT	CT	CT	C	C	C
SL084	+	+	+	C	C	C	GA	G	GA	G	G	G	CT	C	CT	C	C	C
SL111	+/-	+	+/-	CT	C	CT	GA	G	GA	G	G	G	CT	CT	CT	CT	CT	CT
SL097	+	+	+	CT	C	CT	GA	G	GA	G	G	G	CT	C	CT	C	C	C
SL089	+	+	+	C	C	C	GA	GA	GA	GA	GA	GA	CT	CT	CT	C	C	C
SHSY	+/-	+	+/-	CT	C	CT	GA	GA	GA	GA	GA	GA	C	C	C	C	C	C

[illegible]

FIGURE 6

	1						
EXON D	CAGGCCGCCA	CATAGCTCCC	GCCAAGTCCT	CGGTGCCCCCT	TGCCATTTTC	CAGCCGCGTC	CCACGAGGGT
297bp	CACGGCGGCG	GGGAGAGGTG	GAGCCGCGAG	AGCTCGGCCG	GGGGCCCCGC	CTGGTGCCCG	CGGCCATGAC
	AGCGGCTCGG	GACTGGCTCC	TTTTCCGCGC	CCCTCCCCGC	GGAGGTGAGG	GGAAGATGTC	CATGTCAGGG
	TTCAAGGCCA	AACCGAAGTT	ACTGGCCTCT	ATCTTCCAGG	AGAACCAGGA	GCCACAGCCG	CGGCTCACGC
	CCCACCGCAA	CATTAAAGgtg	agtcgcc.....				
		297					
		298					
EXON Cctc	atttcagATT	ACAAGTGGAC	ACCTGAGTCA	GCAGGACCTG	GAATCCCAGA	TGAGAGAGCT
125bp	TATCTACACG	ACTCAGATCT	TGTGTGCACC	CCCATTATTG	ACAATCCAAA	GGTGCAGAAA	GCACTCTGAC
	AAgtgagttg	ta.....					
	422						
		423					
EXON B	..ttaaccac	agATAATGAA	ACAACCACCA	TCGGTTAAAT	TTGATGCAAA	AATATTGCAT	CTACCAGCAT
64bp	TTTCAGgtag	gatcat.....					
	486						
		487					
EXON Attta	ttctagTTCC	AATTGCTAAT	CCAGCATTTG	TGGATAGCTG	CAAACCTGCGA	TATgtaagta
47bp	aca.....						533
		534					
EXON 5	...ctgtttc	tagTGCTGAT	GAGCGCTTTG	ACGCCACATT	CCACACTAAC	GTGTTGGTGA	ATTCTTCTGG
80bp		GCATTGCCAG	TACCTGCCTC	CAGgtaagctgca.....			
				613			
		614					
EXON 6accaca	cagGCATATT	CAAGAGTTCC	TGCTACATCG			
27bp				640			

FIGURE 7

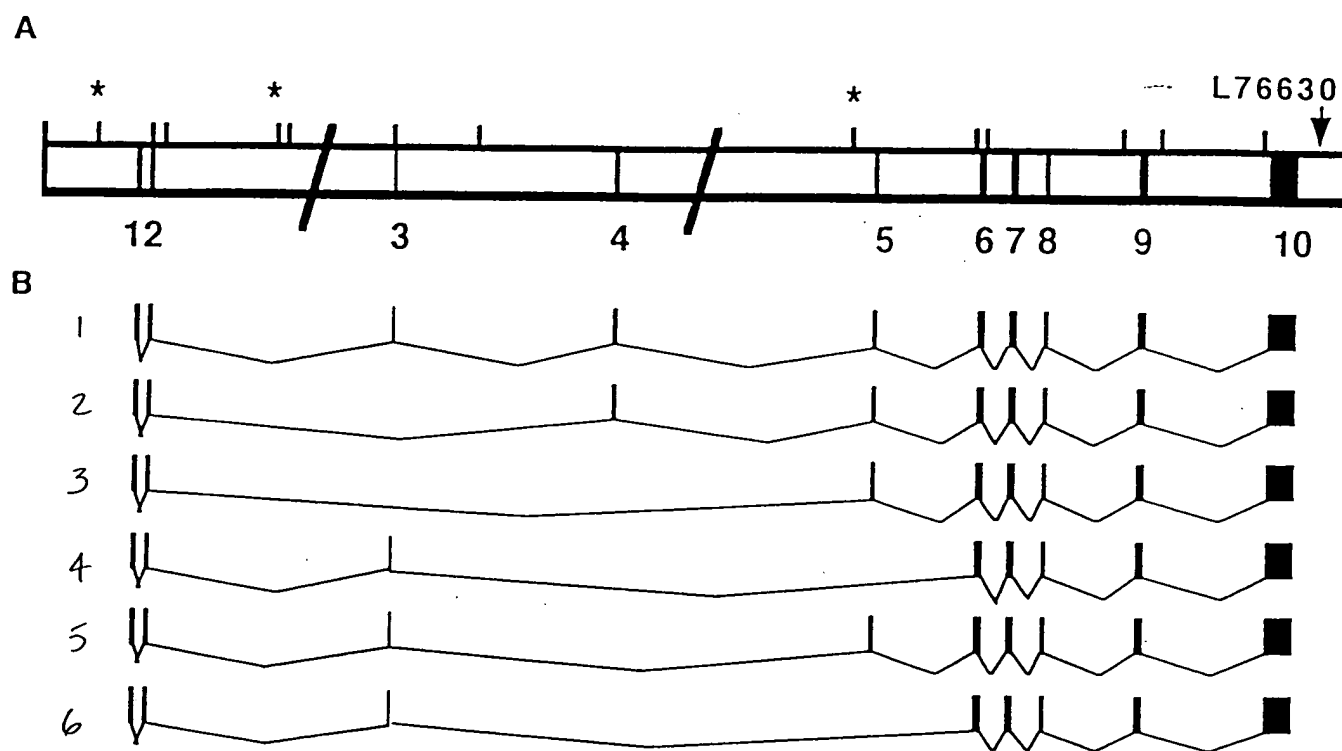


FIGURE 8

1 agaacgcaag ggagaggtag agcctggcct tgggcagccc ctggcctggc cagaggcgcg
61 aggccgagag cccgctcggt ggagactggg ggtggaggtg cccggagcgt acccagcgcc
121 gggagtacct cccgctcaca ctcggggctg cagttccctg ggtggccgcc gagacgctgg
181 cccgggctgg agggatggcg gggcggggac gggggcgggg gcggggctcg tcacgtggag
241 aggcgcgcgg gggcggggcg ggcgggggag cgccccggc tcctaaagg cgcgcgagcc
301 gagcggcgag gtcctctgt ggccgcaggg gcaggcccgg gcgacagccg agacgtggag
361 cgcgccggct cgctgcagct ccgggactca ac

FIGURE 9

1 agccctttcc caggcggtag cggggggcagt ggtgctgtg cccttttaa ctgcggcttg
61 acgggagccg cgcctcctgt cggaggagtc ggtataaag ggagcagccc cgcaggccgc
121 cacatagctc cgcceaagtc ctcggtgccc ctgccattt tccagccgcg ctcccacgag
181 ggtcacggcg gcggggagag gtggagccgc gagagctcg cggggggccc cgcctggtgg
241 ccgcgcccat gacagcggct cgggactggc tcctttccg cggccctccc gccggaggtg
301 aggggaagat gtccatgtca ggggtcaagg ccaaaccgaa gttactggcc tctatctcc
361 aggagaacca ggagccacag ccgcggctca cggccaccg caacattaag attacaagt
421 gacacctgag tcagcaggac ctggaatccc agatgagaga gcttatctac acgactcaga
481 tcttgtgtc accccatta ttgacaatcc aaaggtgcag aaagcactct gacaattcca
541 attgctaac cagcatttgt ggatagctgc aaactgcgat attgctgatg agcgtttga
601 cgccacattc cacactaacg tgttggtgaa ttctctggg cattgccagt acctgcctcc
661 aggcatattc aagagttcct gctacatcg



FIGURE 10

1 caggccgcca catagctccc gccaaagtcct cggtgcccct tgccatttc cagccgcgct
61 cccacgaggg tcacggcggc ggggagaggt ggagccgca gagtcggcc gggggccccg
121 cctggtggcc gcggccatga cagcggctcg ggactggctc ctttccgcg cccctcccgc
181 cggaggtgag ggggaagatgt ccatgtcagg gttaaggcc aaaccgaagt tactggcctc
241 tatcttcag gagaaccagg agccacagcc gcggctcacg cccaccgca acattaagat
301 tacaagtga cacctgagtc agcaggacct ggaatcccag atgagagagc ttatctacac
361 gactcagatc ttgtgtcac cccattatt gacaatcaa aggtgcagaa agcactctga
421 caaataatga aacaaccacc atcgggtaaa ttgatgcaa aaatattgca tctaccagca
481 tttcagttc caattgctaa tccagcattt gtggatagct gcaaactgcg atattgctga
541 tgagcgctti gacgccacat tccacactaa cgtgttggtg aattctctg ggcattgcca
601 gtacctgcct ccaggecatat tcaagagttc ctgctacac g